

10 30 50  
 CTAGAGCTAGCAGGAGTAACCTCATGGAACCTTGGAAACCATTCTCAATTGAATTCA  
 70 90 110  
 GGGCACATTGAATCAGTACCCAGGGGCACTGTACTATGCTCCAGCTGGACCTAGTT  
 130 150 170  
 CCTCCTCTCGTTCACCCCTGTGAGTAATTAAACAGACAAAATTTTTTTTTTTTT  
 190 210 230  
 TTTTTTTTTTTTGCCTCCAGTGGAGAAGGTGGCCAGTCTCAGACAGAGGAAGAGT  
 250 270 290  
 AGAAATCATAAATGAGAGCTGTCTCATCCAAGGTGCTGAAGAGCACCCTGCGGATTCT  
 M R A V F I Q G A E E H P A A F C 17  
 310 330 350  
 GCTACCAGGTGAATGGGCTTGCCTCCAGGACAGTACATACTCTGGCATCCAGTGGTCA  
 Y Q V N G S C P R T V H T L G I Q L V I  
 370 390 410  
 TCTACCTGACCTGTGCAGCAGGCATGCTGATTATCGTGTAGGAAATGTATTGTGGCAT  
 Y L T C A A G M L I I V L G N V F V A F  
 430 450 470  
 TTGCTGTGCTACTTCAAAGCGCTTACACGCCACCAACTCCTGCTGCTCTCCCTGG  
 A V S Y F K A L H T P T N F L L L S L A  
 490 510 530  
 CCCTGGCTGACATGTTCTGGGTCTGCTGGTGTGCCCTCAGCACCATTGCTCAGTGG  
 L A D M F L G L L V L P L S T I R S V E  
 550 570 590  
 AGAGCTGCTGGTTCTCGGGACTTCCTCTGCCGCCTGCACACCTACCTGGACACCCTCT  
 S C W F F G D F L C R L H T Y L D T L F  
 610 630 650  
 TCTGCCTCACCTCCATTTCCATCTCTGTTCATTTCCATTGACCGCCACTGTGCCATCT  
 C L T S I F H L C F I S I D R H C A I C  
 670 690 710  
 GTGACCCCTGCTCTATCCCTCCAAGTTACAGTGAGGGTGGCTCTCAGGTACATCCTGG  
 D P L L Y P S K F T V R V A L R Y I L A  
 730 750 770  
 CAGGATGGGGGTGCCCGCAGCATACACTTCGTTATCCTCTACACAGATGTGGTAGAGA  
 G W G V P A A Y T S L F L Y T D V V E T  
 790 810 830  
 CAAGGCTCAGCCAGTGGCTGGAAGAGATGCCCTGTGTGGCAGTGCCAGTGCTGCTCA  
 R L S Q W L E E M P C V G S C Q L L L N  
 850 870 890  
 ATAAATTGGGGCTGGTAAACTCCCTTGTCTTGTCCCCTGCCCTCATATTGATCA  
 K F W G W L N F P L F F V P C L I M I S  
 910 930 950  
 GCTTGTATGTGAAGATCTTGTGGTTGCTACCAGACAGGCTCAGCAGATTACACATTGA  
 L Y V K I F V V A T R Q A Q Q I T T L S  
 970 990 1010  
 GCAAAAGCCTGGCTGGGCTGCCAAGCATGAGAGAAAAGCTGCCAAGACCCCTGGCATTG  
 K S L A G A A K H E R K A A K T L G I V  
 1030 1050 1070  
 TTGTGGGCATATACCTCTTGTGCTGGCTGCCCTCACCATAGACACGATGGTCGACAGCC  
 V G I Y L L C W L P F T I D T M V D S L  
 1090 1110 1130  
 TCCTTCACTTATCACACCCCCACTGGTCTTGACATCTTATCTGGTTGCTTACTTCA  
 L H F I T P P L V F D I F I W F A Y F N  
 1150 1170 1190  
 ACTCAGCCTGCAACCCCCATCATCTATGTCTTCCCTACCAAGTGGTTCGGAAGGCAGTGA  
 S A C N P I I Y V F S Y Q W F R K A L K  
 1210 1230 1250  
 AACTCACACTGAGCCAGAAGGTCTCTCACCGCAGACACGCAGTGTGATTGTACCAAG  
 L T L S Q K V F S P Q T R T V D L Y Q E  
 1270 1290 1310  
 AATGATTCTTCACTAAATGCAGGCAAGGAGTAGGACCTCACAGGAAAGATAAGTGGCA  
 \*  
 1330 1350 1370  
 CTGTGACCGCGGGCTGTGTGGTGGTGGAGTTGTGGCATGCTCCAGGACAGCATGGTT  
 325800-451

1330 1350 1370  
CTGTGACCGCGGGCTGTGGTGTGAGTTGTGGGCATGCTCCAGGACAGCATGGGTT  
325800-451

Homology Comparison  
HDGRC02 X Mu. $\beta$ -1 Adrenoreceptor

Percent Similarity: 55.864      Percent Identity: 32.099

09982414-42004

3	AVFIQGAEEHPAAFCYQVNGSCPRTVH.TLGIQLVIYLTCAGMLIIVLG	51
30	ARLLVLASPPASLLPPASEGSAPLSQQWTAGMGLLVALI....VLLIVVG	75
52	NVFVAFAVSYFKALHTPTNFLLSLALADMFLGLLVLPLSTIRSVESCFW	101
76	NVLVIVIAIKTPRLQTLTNLFIMSLASADLVMGLLVVPGATIVVWGRWE	125
102	FGDFLCLRLHTYLDTLFCLTSIFHLCFISIDRHCAICDPLLYPSKFTVRVA	151
126	YGSFFCELWTSVDVLCVTASIETLCVIALDRYLAITSPPFRYQSLLTRARA	175
152	LRYILAGWGVPAAYTSFLYTDVVETRLSQWLEEMPCVG...SCQLLLNK	198
176	RALVCTVWAISAL...VSFLPILMHWWRAESDEARRCYNDPKCCDFVTNR	222
199	FWGWLNFPL.FFVPCLIMISLYVKIFVVATRQAQQITTLSKSLAGA....	243
223	AYAIASSVVSFYVPLCIMAFVYLRVFREAQKQVKIDSCERRFLGGPARP	272
244	.....AKHERKAAKTLGIVVGIY	261
273	PSPEPSPSPGPPRPADSLANGRSSKRRPSRLVALREQKALKTLGIIMGVF	322
262	LLCWLPFTIDTMVDSLLHFITPPLVFDIFIWFAYFNSACNPPIIYVFSYQW	311
323	TLCWLPFFLANVVKAFHRDLVPDRLFVFFNWLGYANSAFNPIIYCRSPDF	372
312	FRKALKLTLSQKVFSQPTRTVD	333
373	RKAFQRLLCARRAACRRRAAH	394

FIGURE 2 11  
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## Homology Comparison HDGRC02 X Hu. D2 receptor

Percent Similarity: 58.333 Percent Identity: 32.000

8 GAEHPAAFCYQVN GSCPRTVHTLGIQLVIYLTCAGMLIIVLGNVFVAF 57  
...  
10 DDDLERQNWSRPFNGSDGKADRPHYNYYATLLT..LLIAVIVFGNVLVCM 57  
59 AVSYFKAI.HPTNFLLLSSLALADMFLGLLVLPLSTIRSVESCWFFGDFLC 107  
| | | | | | : | . | | : | : | | : | : | : | : | . | : | : | : |  
58 AVSREKALQTTNYLIVSLAVADLLVATLVMPPWVYLEVVG EWKFSRIHC 107  
108 RLHTYLDTLFCLTSIFHLCFISIDRHCAICDPLLYPSKFTVRVALRYILA 157  
: . | | : | . | | : | | | | . | : | . : | : : | : : : :  
108 DIFVTLDVMMCTASILNLCAISIDRYTAVAMPMLYNTRYSSKRRVTVMIS 157  
158 .GWGVPAAYTSLFLYTDVVETRLSQWLEEMPCVGSCQLLLNLKFWGWLNF 206  
. | . . . . . . : | . | .. : . . . . . . . . . . . . . . . .  
158 IVWVLSFTISCPLLFG.....LNNADQNECIIIANPAFVV.....YSSIV 196  
207 LFFVPCLIMISLYVKIFVVATRQAQQITT.....LSKSLAGAAKH 246  
| : | | : : : | : | : | | . . . . . . . . . . . . . . . .  
197 SFYVPFIVTLLVYIKIYIVLRRRKRVNTKRSSRAFRAHLRAPLKEAARR 246  
247 .....ERKAAKTL 254  
| : | .  
297 EKNGHAKDHPKIAKIFEIQTMPNGKTRTSLKTMSRRKLSQQKEKKATQML 346  
255 GIVVGIYLLCWLPTIDTMVDSLLHFITPPLVFDIFIFIWFAYFNSACNPII 304  
: | | : : : : | | | | | . . . . . . . . . . . . . . . . . .  
347 AIVLGVFIICWLPPFITHILNIHDCCNIPPVLYSAFTWLGYVNSAVNPII 396  
305 YVFSYQWFRKALKLTL 320  
| . | | | : . |  
397 YTTFNIEFRKAFLKIL 412

FIGURE 3  
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